

3/8



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/075,846

DATE: 03/01/2002 P.5
TIME: 11:50:04

Input Set : A:\EP.txt

Output Set: N:\CRF3\03012002\J075846.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA
 SUBUNIT EXPRESSED
 6 IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
 8 <130> FILE REFERENCE: D0079 NP
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/075,846
 C--> 10 <141> CURRENT FILING DATE: 2002-02-13
 10 <150> PRIOR APPLICATION NUMBER: US 60/269,535
 11 <151> PRIOR FILING DATE: 2001-02-16
 13 <160> NUMBER OF SEQ ID NOS: 81
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2565
 19 <212> TYPE: DNA
 20 <213> ORGANISM: homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(1251)
 26 <400> SEQUENCE: 1
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 29 1 5 10 15
 31 ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc 96
 32 Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val
 33 20 25 30
 35 aaa tct gga acc aag ggg tcc cag ccc atg tcc ccc tct gat ttc cta 144
 36 Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu
 37 35 40 45
 39 gac aaa ctt atg ggg cga aca tct gga tat gat gcc agg att cgg ccc 192
 40 Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro
 41 50 55 60
 43 aat ttt aaa ggc cca ccc gtg aac gtg acc tgc aac atc ttc atc aac 240
 44 Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn
 45 65 70 75 80
 47 agt ttc agc tcc gtc acc aag acc aca atg gac tac cgg gtg aat gtc 288
 48 Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp Tyr Arg Val Asn Val
 49 85 90 95
 51 ttc ttg cgg caa cag tgg aat gac cca cgc ctg tcc tac cga gaa tat 336
 52 Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr
 53 100 105 110
 55 cct gat gac tct ctg gac ctc gat ccc tcc atg ctg gac tct atc tgg 384
 56 Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp
 57 115 120 125
 59 aag cca gac ctc ttc ttt gct aat gag aaa ggg gcc aac ttc cat gag 432

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61		130					135					140					
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64	Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe	Lys	Asn	Gly	Asn	Val	
65	145					150					155					160	
67	ctg	tac	agc	atc	agg	ctg	acc	ctc	att	ttg	tcc	tgc	ctg	atg	gac	ctc	528
68	Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Ile	Leu	Ser	Cys	Leu	Met	Asp	Leu	
69					165					170					175		
71	aag	aac	ttc	ccc	atg	gac	atc	cag	acc	tgc	acg	atg	cag	ctt	gag	agc	576
72	Lys	Asn	Phe	Pro	Met	Asp	Ile	Gln	Thr	Cys	Thr	Met	Gln	Leu	Glu	Ser	
73				180					185					190			
75	ttt	ggc	tac	acc	atg	aaa	gac	ctc	gtg	ttt	gag	tgg	ctg	gaa	gat	gct	624
76	Phe	Gly	Tyr	Thr	Met	Lys	Asp	Leu	Val	Phe	Glu	Trp	Leu	Glu	Asp	Ala	
77			195					200					205				
79	cct	gct	gtc	caa	gtg	gct	gag	ggg	ctg	act	ctg	ccc	cag	ttt	atc	ttg	672
80	Pro	Ala	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	
81		210					215					220					
83	cgg	gat	gag	aag	gat	cta	ggc	tgt	tgt	acc	aag	cac	tac	aac	aca	ggg	720
84	Arg	Asp	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	
85	225				230					235						240	
87	aaa	ttc	acc	tgc	atc	gag	gta	aag	ttt	cac	ctg	gaa	cgg	cag	atg	ggc	768
88	Lys	Phe	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	
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91	tac	tat	ctg	att	cag	atg	tac	atc	ccc	agc	cta	ctc	atc	gtc	atc	ctg	816
92	Tyr	Tyr	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	
93			260					265					270				
95	tcc	tgg	gtc	tcc	ttc	tgg	atc	aac	atg	gat	gct	gcc	cct	gcc	cgt	gtg	864
96	Ser	Trp	Val	Ser	Phe	Trp	Ile	Asn	Met	Asp	Ala	Ala	Pro	Ala	Arg	Val	
97			275				280					285					
99	ggc	ctg	ggc	atc	acc	acc	gtg	ctc	acc	atg	acc	acc	cag	agc	tct	ggc	912
100	Gly	Leu	Gly	Ile	Thr	Thr	Val	Leu	Thr	Met	Thr	Thr	Gln	Ser	Ser	Gly	
101		290					295					300					
103	tcc	cgg	gcc	tct	ttg	cct	aag	gtg	tcc	tac	gtg	aag	gca	atc	gac	atc	960
104	Ser	Arg	Ala	Ser	Leu	Pro	Lys	Val	Ser	Tyr	Val	Lys	Ala	Ile	Asp	Ile	
105	305				310					315						320	
107	tgg	atg	gct	gtg	tgt	ctg	ctc	ttt	gtg	ttc	gct	gcc	ttg	ctg	gag	tat	1008
108	Trp	Met	Ala	Val	Cys	Leu	Leu	Phe	Val	Phe	Ala	Ala	Leu	Leu	Glu	Tyr	
109				325					330					335			
111	gct	gcc	ata	aat	ttt	gtt	tct	cgt	cag	cat	aaa	gaa	ttc	ata	cga	ctt	1056
112	Ala	Ala	Ile	Asn	Phe	Val	Ser	Arg	Gln	His	Lys	Glu	Phe	Ile	Arg	Leu	
113			340					345					350				
115	cga	aga	agg	cag	agg	cgc	caa	cgc	ttg	gag	gaa	gat	atc	atc	caa	gaa	1104
116	Arg	Arg	Arg	Gln	Arg	Arg	Gln	Arg	Leu	Glu	Glu	Asp	Ile	Ile	Gln	Glu	
117			355				360					365					
119	agt	cgt	ttc	tat	ttc	cgt	ggc	tat	ggc	ttg	ggc	cac	tgc	ctg	cag	gca	1152
120	Ser	Arg	Phe	Tyr	Phe	Arg	Gly	Tyr	Gly	Leu	Gly	His	Cys	Leu	Gln	Ala	
121		370				375					380						
123	aga	gat	gga	ggt	cca	atg	gaa	ggt	tct	ggc	att	tat	agt	ccc	caa	cct	1200
124	Arg	Asp	Gly	Gly	Pro	Met	Glu	Gly	Ser	Gly	Ile	Tyr	Ser	Pro	Gln	Pro	

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125 385          390          395          400
127 cca gcc cct ctt cta agg gaa gga gaa acc acg cgg aaa ctc tac gtg      1248
128 Pro Ala Pro Leu Leu Arg Glu Gly Glu Thr Arg Lys Leu Tyr Val
129          405          410          415
131 gac tgagccaaga gaattgacac catctcccgg gctgtcttcc ctttcacttt      1301
132 Asp
135 cctcatcttc aatatcttct actgggttgt ctataaagtg ctacgggtcag aagatatcca      1361
137 ccaggctctg tgaatagggg gggagctata gagtccctgt gctggcctcc tgcttccctcc      1421
139 tgggtgggct ttctccctca gttagactcc attaggggtt tggacagttc cttcctgac      1481
141 tcccactcag aacttcaact accagtccca aagctatgtg ggcctatatt gcatgggtgcc      1541
143 aatgggtggc gtacttataa agatggctta tctaccctag tccatatttt ctccatactt      1601
145 tccattttct catgagacta aggtttggcc acattcctgg ggccaggatg accttctgcc      1661
147 cttgctggag cctccctgtt ttccaatact ccagtggaga gtattcagaa cactgctgct      1721
149 agattctggc atttgtcacc ttaatctgca ccacttctcc ccctgccacc tcccaccag      1781
151 agcctggcca ttactctgtc ctctgtccct cctgctgcag attcaaagtg tgagtttctc      1841
153 ctatccacaa gtgctgccct gtggggccta gtcaggtttc cttgaagtga gaggaaggca      1901
155 aagccgcaag ttccccacct ctcgagaggg ttggaacagt cataggctgc actgggctag      1961
157 cgactatatg gcccaacaga gaggtgttca agtctcttgg gaagccccac actttgtctt      2021
159 catccctttt cctattgcgc ttgtctgtc tttcctgttc actgagatac tcctcttgtc      2081
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163 tgtcagaatt ggggcagaga ctttgggttc tcaaaaagac taacctcca gatccacctg      2201
165 aacattctgg tctcagaaat attcgttccg ttccctaatt aactagcatg gtggcaggat      2261
167 ctgttggaca gctggggagt gtaaaaaaag aaaaatactt gttctttaag aaacttactt      2321
169 tatgatgcta gaaaactttt gagaaaagtg agatccaagg tagtgaacc caggaggagt      2381
171 agaatagaga aactattctc agagtgtctt ttgttggctg ggctttcatt tgtttcttct      2441
173 ttctcaccaa agtctatttt ccagggccct tcatttccaa cctggtcttt cacctccttt      2501
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182 <212> TYPE: PRT
183 <213> ORGANISM: homo sapiens
185 <400> SEQUENCE: 2
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192          20          25          30
195 Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu
196          35          40          45
199 Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro
200          50          55          60
203 Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn
204 65          70          75          80
207 Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp Tyr Arg Val Asn Val
208          85          90          95
211 Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr
212          100          105          110
215 Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp
216          115          120          125

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224 145      150      155      160
227 Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu
228      165      170      175
231 Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser
232      180      185      190
235 Phe Gly Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala
236      195      200      205
239 Pro Ala Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu
240      210      215      220
243 Arg Asp Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly
244 225      230      235      240
247 Lys Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly
248      245      250      255
251 Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu
252      260      265      270
255 Ser Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val
256      275      280      285
259 Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly
260      290      295      300
263 Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile
264 305      310      315      320
267 Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr
268      325      330      335
271 Ala Ala Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu
272      340      345      350
275 Arg Arg Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu
276      355      360      365
279 Ser Arg Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala
280      370      375      380
283 Arg Asp Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro
284 385      390      395      400
287 Pro Ala Pro Leu Leu Arg Glu Gly Glu Thr Arg Lys Leu Tyr Val
288      405      410      415
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296 <211> LENGTH: 1640
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307 1      5      10      15
309 ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc      96

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310	Leu	Pro	Gly	Gln	Val	Leu	Leu	Arg	Val	Ala	Leu	Ala	Lys	Glu	Glu	Val	
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314	Lys	Ser	Gly	Thr	Lys	Gly	Ser	Gln	Pro	Met	Ser	Pro	Ser	Asp	Phe	Leu	
315			35					40					45				
317	gac	aaa	ctt	atg	ggg	cga	aca	tct	gga	tat	gat	gcc	agg	att	cgg	ccc	192
318	Asp	Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp	Ala	Arg	Ile	Arg	Pro	
319		50					55					60					
321	aat	ttt	aaa	ggc	cca	ccc	gtg	aac	gtg	acc	tgc	aac	atc	ttc	atc	aac	240
322	Asn	Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys	Asn	Ile	Phe	Ile	Asn	
323	65					70				75				80			
325	agt	ttc	agc	tcc	gtc	acc	aag	acc	aca	atg	gac	tac	cgg	gtg	aat	gtc	288
326	Ser	Phe	Ser	Ser	Val	Thr	Lys	Thr	Thr	Met	Asp	Tyr	Arg	Val	Asn	Val	
327					85					90				95			
329	ttc	ttg	cgg	caa	cag	tgg	aat	gac	cca	cgc	ctg	tcc	tac	cga	gaa	tat	336
330	Phe	Leu	Arg	Gln	Gln	Trp	Asn	Asp	Pro	Arg	Leu	Ser	Tyr	Arg	Glu	Tyr	
331				100					105					110			
333	cct	gat	gac	tct	ctg	gac	ctc	gat	ccc	tcc	atg	ctg	gac	tct	atc	tgg	384
334	Pro	Asp	Asp	Ser	Leu	Asp	Leu	Asp	Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp	
335			115				120						125				
337	aag	cca	gac	ctc	ttc	ttt	gct	aat	gag	aaa	ggg	gcc	aac	ttc	cat	gag	432
338	Lys	Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly	Ala	Asn	Phe	His	Glu	
339		130				135						140					
341	gtg	acc	acg	gac	aac	aag	tta	ctg	cgc	atc	ttc	aag	aat	ggg	aat	gtg	480
342	Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe	Lys	Asn	Gly	Asn	Val	
343	145				150					155				160			
345	ctg	tac	agc	atc	agg	ctg	acc	ctc	att	ttg	tcc	tgc	ctg	atg	gac	ctc	528
346	Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Ile	Leu	Ser	Cys	Leu	Met	Asp	Leu	
347				165					170					175			
349	aag	aac	ttc	ccc	atg	gac	atc	cag	acg	tgc	acg	atg	cag	ctt	gag	agc	576
350	Lys	Asn	Phe	Pro	Met	Asp	Ile	Gln	Thr	Cys	Thr	Met	Gln	Leu	Glu	Ser	
351				180				185					190				
353	tca	tcc	ata	ctc	tgc	agc	cct	ctg	cca	tct	ctg	tca	ctt	tca	gtt	ggc	624
354	Ser	Ser	Ile	Leu	Cys	Ser	Pro	Leu	Pro	Ser	Leu	Ser	Leu	Ser	Val	Gly	
355			195				200						205				
357	tac	acc	atg	aaa	gac	ctc	gtg	ttt	gag	tgg	ctg	gaa	gat	gct	cct	gct	672
358	Tyr	Thr	Met	Lys	Asp	Leu	Val	Phe	Glu	Trp	Leu	Glu	Asp	Ala	Pro	Ala	
359		210					215					220					
361	gtc	caa	gtg	gct	gag	ggg	ctg	act	ctg	ccc	cag	ttt	atc	ttg	cgg	gat	720
362	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	Arg	Asp	
363	225				230					235				240			
365	gag	aag	gat	cta	ggc	tgt	tgt	acc	aag	cac	tac	aac	aca	ggg	aaa	ttc	768
366	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	Lys	Phe	
367				245					250				255				
369	acc	tgc	atc	gag	gta	aag	ttt	cac	ctg	gaa	cgg	cag	atg	ggc	tac	tat	816
370	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	Tyr	Tyr	
371				260				265					270				
373	ctg	att	cag	atg	tac	atc	ccc	agc	cta	ctc	atc	gtc	atc	ctg	tcc	tgg	864
374	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	Ser	Trp	

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12